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NOTES ON GEOGRAPHIC DISTRIBUTION

Range extension of Blackstripe Lizardfish, *Synodus nigrotaeniatus* Allen, Erdmann & Peristiwady, 2017 (Actinopterygii, Aulopiformes, Synodontidae), from Jakarta Bay, Indonesia

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Abstract. Three specimens (194.4–203.8 mm standard lengths) of the lizardfish *Synodus nigrotaeniatus* Allen, Erdmann & Peristiwady, 2017, collected from Jakarta Bay, western Indonesia, represent a significant range extension for the species, which was previously known from only six specimens collected in Lembeh Strait, North Sulawesi, eastern Indonesia. Morphological comparisons with available data from the type specimens and molecular data from the mitochondrial cytochrome oxidase subunit I (COI) gene are presented. The COI sequence data show a 4% genetic difference from the related *Synodus sageneus* Waite, 1905.

Key words. COI, distribution, morphology, voucher specimens, western Indonesia

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INTRODUCTION

The genus *Synodus* Scopoli, 1777 (Teleostei, Synodontidae) is characterized by having eight pelvic fin rays, with the innermost ones longer than the outermost, 8–11 anal fin rays, with the fin base length shorter than the dorsal-fin base (except *Synodus nigrotaeniatus* Allen, Erdmann & Peristiwady, 2017 and *Synodus sageneus* Waite, 1905), and the procurrent caudal-fin rays not covered by scales (Cressey 1981; Russell 1999). *Synodus* comprises 47 valid species, including 35 Indo-Pacific species, and six species each in the eastern Pacific and Atlantic oceans (Fricke et al. 2024). In Indonesian waters, the genus is currently known from 13 species (Allen and Adrim 2003; Allen and Erdmann 2012; Allen et al. 2017), although the recently described *S. nigrotaeniatus* has been reported only from the type locality in Lembeh Strait, North Sulawesi Province, eastern Indonesia (Allen et al. 2017).

Three lizardfish specimens were recently collected by local fishermen as bycatch from Jakarta Bay, western Indonesia, and subsequently identified as Blackstripe Lizardfish, *S. nigrotaeniatus*, represent the first record of the species from western Indonesian waters. Comparisons between the specimens with available data from the six type specimens of the species are provided, along with molecular data from the mitochondrial cytochrome oxidase subunit I (COI).

METHODS

Counts and measurements followed Allen et al. (2017). Standard length is expressed as SL. Vertebral numbers were counted from radiographs taken using the portable x-ray apparatus Collimax X-ray Collimator R-120 H. Sex was confirmed by dissection of the right side of the abdomen. Curatorial procedures for the specimens [deposited at the Museum Zoologicum Bogoriense, Indonesia (MZB)] followed Motomura and Ishikawa (2013).

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Tissue samples were collected from muscle and extracted following Chelex 10% protocols (Walsh et al. 1991). Extracted DNA was amplified by Polymerase Chain Reaction (PCR) targeting the cytochrome oxidase subunit 1 (COI) with forward primer JgLCO 5′-TITCIACI AAYCAYAARGAYATTGG-3′ and reverse primer JgHCO 5′-TAIACYTCIGGRTGICCRAARAAYCA3′ (Geller et al. 2013). The PCR reaction was carried out in 25 µL volumes, using 4 µL of DNA template. Each reaction included 12.5 µL MyTaqTM Red Mix (Bioline), 1 µL of each primer, and 6.5 µL ddH2O. The thermocycling profile included initial denaturation of 95 °C for 4 min, 40 cycles of 95 °C for 30 s, 50 °C for 30 s, and 72 °C for 1 min, with a final extension at 72°C for 10 min. The PCR reactions were checked on 1% agarose gel stained with Florosafe (1st BASE, Singapore), the results being visualized using a UV-transilluminator and documented with a digital camera. Amplicons were then sequenced using the Sanger Sequencing Platform.

Forward and reverse sequences were checked, cleaned, and aligned using MEGA X software (Kumar et al. 2018) and then compared to the open database of NCBI (The National Center for Biotechnology Information; https://www.ncbi.nlm.nih.gov) using BLAST (Basic Local Alignment Search Tool; https://blast.ncbi.nlm.nih.gov/Blast.cgi). Data for nine species of *Synodus*: *Synodus variegatus* (Lacepède, 1803) (OQ387587.1, OQ385629.1, OQ386861.1); *Synodus jaculum* Russell & Cressey, 1979 (OQ386143.1, OQ386016.1, OQ387075.1); *Synodus dermatogenys* Fowler, 1912 (OQ386222.1); *Synodus tectus* Cressey, 1981 (GU673292.1, GU673291.1, GU673290.1); *Synodus synodus* (Linnaeus, 1758) (HM390092.1, HQ987867.1, GU225063.1); *Synodus rubromarmoratus* Russell & Cressey, 1979 (OQ387399.1, OQ387293.1, OQ386840.1); *Synodus oculeus* Cressey, 1981 (OQ386807.1); *S. sageneus* (GU673294.1, GU673293.1); and *Synodus foetens* (Linnaeus, 1766) (MT455807.1, MT455718.1, MT455242.1) were downloaded from NCBI and used for phylogenetic reconstruction as an aid for understanding the interrelationships of the species of *Synodus*. Sequences of *Trachinocephalus trachinus* (Temminck & Schlegel, 1846) (OQ199052.1) and *Trachinocephalus gauguini* Fernandez, Acero & Betancur, 2016 (MG751098.1) were used as outgroups. A phylogenetic tree was reconstructed using maximum-likelihood analysis, using the HKY+G+I parameter model with 1,000 bootstrap replicas to assess clade support. The maximum-likelihood model and genetic distances with Kimura-2 Parameter model between and within species were calculated with MEGA X (Kumar et al. 2018).

RESULTS

***Synodus nigrotaeniatus* Allen, Erdmann & Peristiwady, 2017**
English common name: Blackstripe Lizardfish
Figures 1, 2, Tables 1, 2

New records. INDONESIA – JAKARTA • Java Sea, Jakarta Bay; 05°57′59″S, 106°43′01″E; 5.XI.2022 and 16.III.2023; K. Wibowo; purchased at Tanjung Pasir Fish Landing Port, Banten Province, Indonesia; 3 ♀; MZB 26876 (NCBI OR730529.1), 198.2 mm SL, MZB 26877 (NCBI OR730530.1), 194.4 mm SL, MZB 26878, 203.8 mm SL.

Identification. The newly collected specimens (Figure 1) from Jakarta Bay, Indonesia were identified as *S. nigrotaeniatus* and closely agree with the diagnostic characters of the species as given by Allen et al. (2017): 12 or 13 dorsal-fin rays; 12–14 anal-fin rays; 12 or 13 pectoral-fin rays; 49 or 50 lateral-line scales; 49 total vertebrae; snout length greater than eye diameter, its length 6.0–6.5% of SL (21.9–23.1% of HL); inter-orbital space 3.7–4.0% of SL; anal-fin base length 17.8–20.2% of SL; a deep suborbital pore with prominent surrounding fimbriae; adipose fin tiny or absent; and preserved and fresh coloration mottled brown dorsally and whitish ventrally, with a distinct blackish strip along the mid-lateral body surface (Figure 1, Table 1).

The COI gene sequences from the two samples acquired in this study (the first reported for *S. nigrotaeniatus*) were successfully amplified by PCR, the total lengths of the sequences are 657 base pairs (bp). The BLAST analysis (Figure 2) indicates a 96% percent similarity with *S. sageneus*; the genetic distance between *S. nigrotaeniatus* and all available species of *Synodus* ranging from 0.042–0.249 (Table 2).

DISCUSSION

Since its original description by Allen et al. (2017), *Synodus nigrotaeniatus* has not been reported from any other locations, including the type locality. Therefore, the discovery of *S. nigrotaeniatus* from Jakarta Bay, approximately 2,200 km southwest of Lembeh Strait, Sulawesi Island (Figure 3), represents a significant range extension, and brings the total number of known examples of the species to nine specimens.

Synodus nigrotaeniatus is most similar to the Indo-West Pacific *S. sageneus*; these two species differ from all other *Synodus* species in having a relatively robust body with the eyes more dorsally directed, a more gradually angled snout profile, a long anal-fin base (its length greater than the dorsal-fin base), a greater number of anal-fin rays, a tiny adipose fin, and a prominent suborbital pore with surrounding fimbriae. However, *S. nigrotaeniatus* differs from *S. sageneus* in several meristic and morphometric characters, and color pattern (Allen et al. 2017).

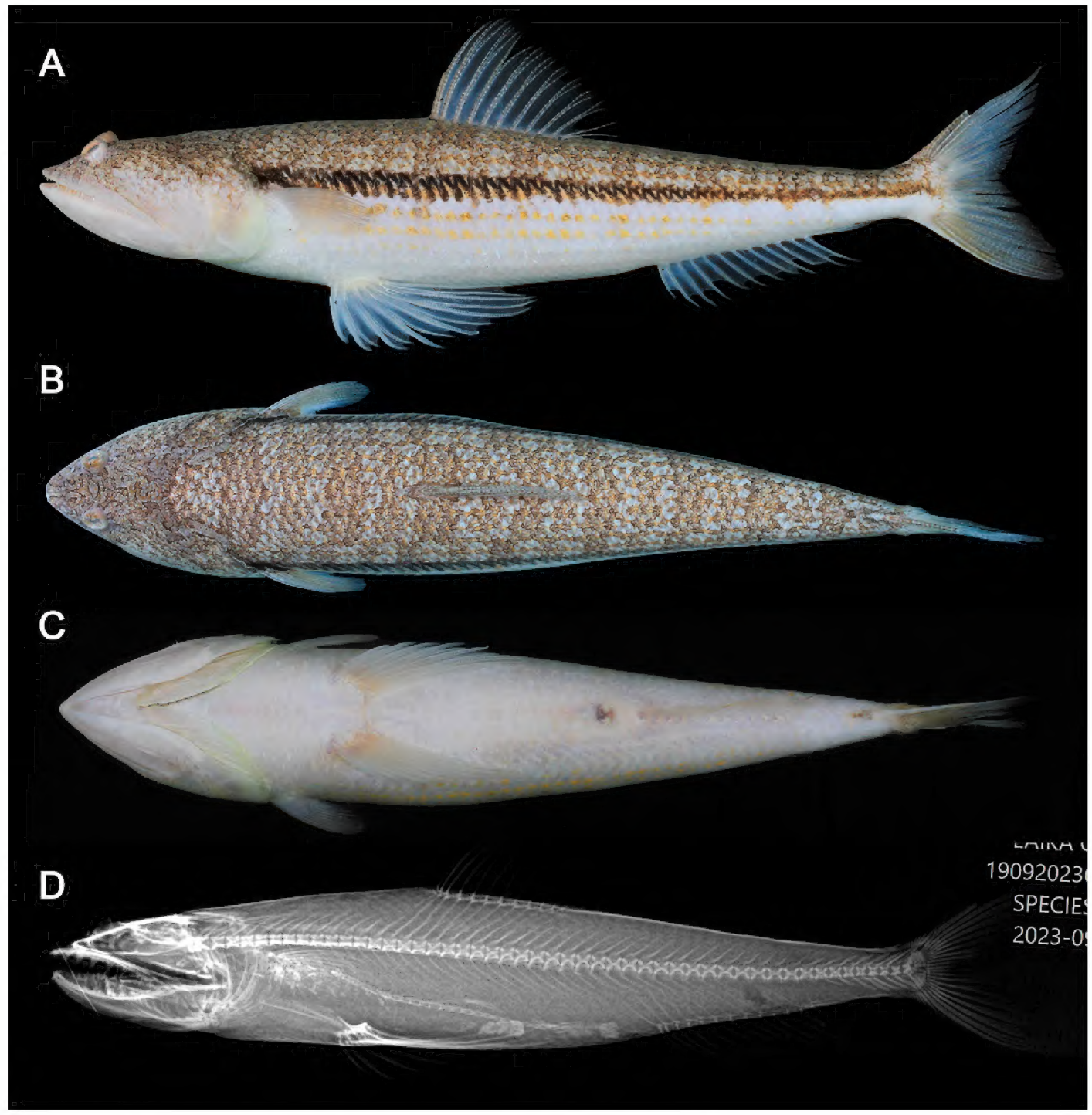

Figure 1. *Synodus nigrotaeniatus*, MZB.26878, 203.8 mm SL, collected from Jakarta Bay, Indonesia. **A.** Lateral view. **B.** Dorsal view. **C.** Ventral view. **D.** Radiograph (lateral).

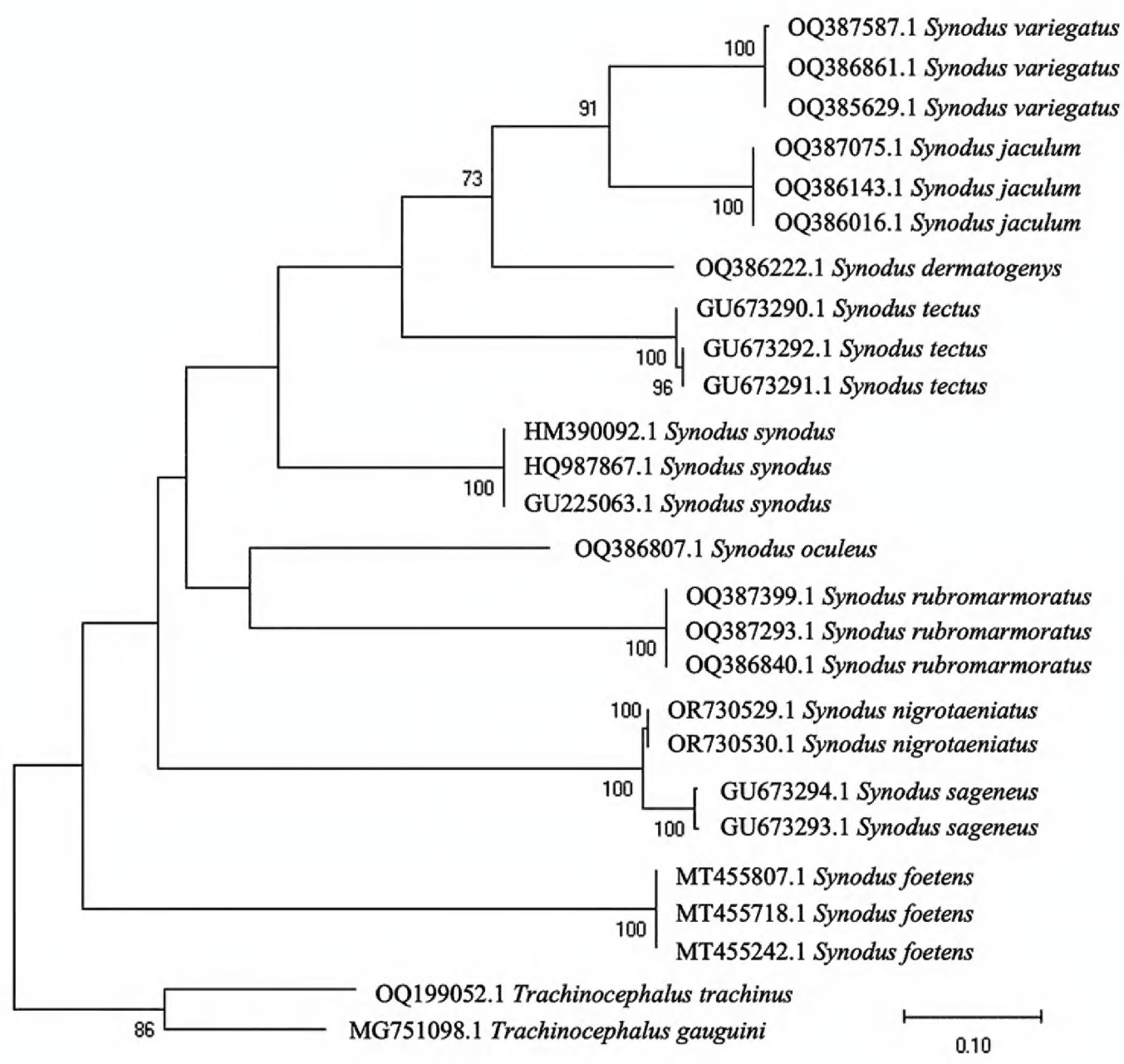

Figure 2. Phylogenetic tree of *Synodus nigrotaeniatus* with maximum-likelihood (ML) topology generated from mtDNA COI gene. Numbers below major nodes indicate maximum likelihood bootstrap support for 1,000 replicates.

Table 1. Counts and measurements (expressed as percentages of standard length) of *Synodus nigrotaeniatus*.

	Allen et al. (2017)		This study, non-types		
	Holotype, LBRC F-3773	**Paratypes, *n* = 5**	**MZB. 26876**	**MZB. 26877**	**MZB. 26878**
Standard length (mm)	233.5	129.7–227.0	198.2	194.4	203.8
Counts					
Dorsal-fin rays	12	11–12	13	12	12
Anal-fin rays	14	12–14	13	14	12
Pectoral-fin rays	13	13	13	12	12
Pevic-fin rays	8	8	8	8	8
Lateral-line scales	48	47–49	50	49	49
Total vertebrae	—	48–49	49	49	49
Measurements (% SL)					
Body depth (at pelvic fin origin)	18.5	15.1–16.5	15.4	20.0	17.0
Body depth (at anal fin origin)	12.8	11.6–12.9	11.9	14.1	12.5
Body width	16.0	14.8–16.8	15.5	16.5	18.0
Head length	27.5	27.6–30.0	27.5	28.2	28.2
Snout length	6.0	6.3–7.1	6.0	6.5	6.2
Orbit diameter	3.2	3.2–3.9	3.0	3.3	3.0
Interorbital width	4.7	3.8–4.9	3.7	4.0	3.8
Upper jaw length	19.3	16.3–20.0	16.7	17.7	17.5
Caudal peduncle depth	5.7	5.1–6.0	5.6	5.8	5.5
Caudal peduncle length	10.2	10.3–14.7	13.6	12.6	13.2
Predorsal fin length	43.0	42.0–45.1	42.4	43.5	43.6
Preanal fin length	69.2	67.3–71.8	69.3	67.9	68.4
Pre-adipose fin length	81.4	80.9–82.1	—	—	—
Pre-pelvic fin length	34.8	33.8–36.6	32.8	34.2	34.1
Dorsal-fin base length	16.1	13.8–15.5	14.6	14.8	14.7
Longest dorsal-fin ray	13.2	12.6–16.3	12.9	12.9	13.6
Anal-fin base length	19.4	17.1–19.6	17.9	20.2	17.8
Longest anal-fin ray length	7.0	6.8–7.6	6.8	6.8	6.9
Caudal fin length	17.3	15.1–17.8	16.7	17.7	18.0
Caudal concavity	6.9	5.0–10.4	9.8	9.4	9.1
Pectoral fin length	12.9	13–14.9	12.2	13.2	12.7
Pelvic fin length	24.8	24.1–27.5	23.7	24.2	24.1

Table 2. Genetic distance between 10 species of the genus *Synodus* and two species of *Trachinocephalus* (outgroups).

No.	Species	1	2	3	4	5	6	7	8	9	10	11	12
1	*S. nigrotaeniatus*	0.000											
2	*S. sageneus*	0.042	0.000										
3	*S. synodus*	0.231	0.240	0.000									
4	*S. variegatus*	0.231	0.213	0.229	0.000								
5	*S. rubromarmoratus*	0.249	0.244	0.217	0.232	0.000							
6	*S. jaculum*	0.221	0.217	0.213	0.136	0.229	0.000						
7	*S. oculeus*	0.224	0.222	0.211	0.236	0.219	0.221	0.000					
8	*S. dermatogenys*	0.239	0.227	0.184	0.171	0.247	0.179	0.215	0.000				
9	*S. tectus*	0.241	0.246	0.194	0.215	0.209	0.204	0.236	0.200	0.000			
10	*S. foetens*	0.242	0.259	0.263	0.232	0.286	0.242	0.252	0.244	0.278	0.000		
11	*T. trachinus*	0.282	0.278	0.249	0.264	0.239	0.228	0.220	0.232	0.229	0.215	0.000	
12	*T. gauguini*	0.234	0.239	0.228	0.278	0.254	0.231	0.231	0.219	0.228	0.272	0.167	0.000

Figure 3. Distributional records of *Synodus nigrotaeniatus* (open and closed stars indicate previous record based on Allen et al. (2017) and present report in this study, respectively).

Several morphometric features (Table 1: body depths at the anal and pelvic fin origins, body width, orbit diameter, interorbital width, pre-pelvic fin length, anal-fin base length, and caudal, pectoral, and pelvic fin lengths) of the newly collected specimens were slightly outside (<1.5% of SL) the ranges of the type specimens of *S. nigrotaeniatus* reported by Allen et al. (2017). In addition, the only meristic differences between the latter and those from Jakarta Bay were dorsal fin ray (11–12 in the former vs. 12–13 in the latter) and lateral-line scale (47–49 vs. 49–50) numbers, both regarded here as intraspecific variation.

However, an inconsistency in the number of pectoral-fin rays was noted in the original description of the species, 11 being indicated in the diagnosis and 13 in the description (Allen et al. 2017). The present specimens suggest that the latter was, in fact, the correct number.

Dissection of the Jakarta Bay specimens (194.4–203.8 mm SL) confirmed their status as mature females, each having an expanded gonad with relatively large eggs.

The molecular data from the COI gene indicated a clear distinction between *S. nigrotaeniatus* and *S. sageneus*, with 4% genetic difference (Table 2), which is equivalent to the percentage difference used to differentiate between many other related reef fish species, such as the *Chrysiptera* species complex (Allen et al. 2015, 2017).

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ADDITIONAL INFORMATION

Conflict of interest

The authors declare that no competing interests exist.

Ethical statement

No ethical statement is reported.

Author contributions

Conceptualization: KW. Data curation: NKDC, MA. Funding acquisition: KW, NKDC. Methodology: SL, GW, SO, RVK. Visualization: GW, SO, RVK. Writing - original draft: NKDC, MA. Writing - review and editing: KW, SL, MA, GW, SO, RVK. Validation: KW, NKDC, SL.

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Data availability

All data that support the findings of this study are available in the main text.

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